

Fri Dec 3 11:48:18 2004

10024369-3_1018-1037sl.rnpb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:43:49 ; Search time 0.001 Seconds
(without alignments)
21.120 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20

Sequence: 1 cttctgcccaagaagtcg99 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 50 segs, 528 residues

Total number of hits satisfying chosen parameters: 100

Minimum DB seg length: 8
Maximum DB seg length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rnpbdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-10-024-369-47
2	12.8	64.0	17	1	US-09-930-423-674
3	12.8	64.0	17	1	US-09-745-237A-674
4	12	60.0	15	1	US-09-775-818-2
5	12	60.0	15	1	US-10-663-999-2
6	9.4	47.0	12	1	US-10-661-165-445
7	9	45.0	10	1	US-10-033-145-410
8	9	45.0	10	1	US-10-033-145-930
9	9	45.0	10	1	US-10-033-145-1231
10	9	45.0	10	1	US-09-862-847-15
11	8.4	42.0	10	1	US-10-033-145-262
12	8.4	42.0	10	1	US-10-033-145-437
13	8.4	42.0	10	1	US-10-033-145-2061
14	8.4	42.0	10	1	US-10-057-726-3
15	8.4	42.0	10	1	US-10-330-627-713
16	8.4	42.0	10	1	US-10-293-222-330
17	8.4	42.0	10	1	US-10-660-253-84
18	8.4	42.0	10	1	US-10-670-011-398
19	8.4	42.0	11	1	US-09-772-719-73
20	8.4	42.0	11	1	US-09-667-237-73
21	8.4	42.0	11	1	US-10-450-797-170
22	8.4	42.0	11	1	US-10-450-797-1255
23	8.4	42.0	11	1	US-10-450-797-1259
24	8.4	42.0	11	1	US-09-989-789-2078
25	8.4	42.0	9	1	US-09-989-789-2079
26	8.4	42.0	9	1	US-09-989-789-2262
27	8.4	42.0	9	1	US-09-989-789-2263
28	8.4	42.0	9	1	US-09-846-033B-7
29	8.4	42.0	9	1	US-09-990-186-2078
30	8.4	42.0	9	1	US-09-990-186-2079
31	8.4	42.0	9	1	US-09-990-186-2262
32	8.4	42.0	9	1	US-09-990-186-2263
33	8.4	42.0	9	1	US-09-989-994-2078

34	8	40.0	9	1	US-09-989-994-2079	Sequence 2079, Ap
35	8	40.0	9	1	US-09-989-994-2262	Sequence 2262, Ap
36	8	40.0	9	1	US-09-989-994-2263	Sequence 2263, Ap
37	8	40.0	9	1	US-10-006-069A-7	Sequence 7, Appl1
38	8	40.0	10	1	US-10-033-145-198	Sequence 198, App
39	8	40.0	10	1	US-10-033-145-196	Sequence 296, App
40	8	40.0	10	1	US-10-033-145-398	Sequence 298, App
41	8	40.0	10	1	US-10-033-145-701	Sequence 701, App
42	8	40.0	10	1	US-10-033-145-1370	Sequence 1370, Ap
43	8	40.0	10	1	US-10-033-145-1792	Sequence 1792, Ap
44	8	40.0	10	1	US-10-033-145-1806	Sequence 1806, Ap
45	8	40.0	10	1	US-10-033-145-1979	Sequence 1979, Ap
46	8	40.0	10	1	US-10-010-602-281	Sequence 281, App
47	8	40.0	10	1	US-10-330-627-132	Sequence 132, App
48	8	40.0	10	1	US-10-330-627-1157	Sequence 1157, Ap
49	8	40.0	10	1	US-10-293-222-324	Sequence 324, App
50	8	40.0	10	1	US-10-215-982-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-10-024-369-47/c
Sequence 47, Application US/10024369
Publication No. US20030134809A1
GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
FILE REFERENCE: RFS-0353
CURRENT APPLICATION NUMBER: US/10/024,369
CURRENT FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 47
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-47

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 20; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 CTTCTGCCCAAGAAGTGCG 1037
Db 20 CTTCTGCCCAAGAAGTGCG 1

RESULT 2
US-09-930-423-674
Sequence 674, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blact, Larry
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MEMBO 918-A, 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO 674
LENGTH: 17
TYPE: RNA
ORGANISM: Homo Sapiens
US-09-930-423-674
Query Match 64.0%; Score 12.8; DB 1; Length 17;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:41:56 ; Search time 0.001 Seconds

(without alignments)
14.120 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20

Sequence: 1 cttctgcccagaagatg99 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 0.5

Searched: 36 segs, 353 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : rn1db:*

Listing first 36 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	45.0	11	US-09-862-847-15	Sequence 15, Appl
2	45.0	12	US-09-862-844-6	Sequence 6, Appl
3	45.0	10	US-09-862-844-8	Sequence 8, Appl
4	42.0	12	US-08-410-7798-47	Sequence 47, Appl
5	42.0	10	US-09-508-7538-225	Sequence 225, App
6	42.0	10	PCT-US95-04477-47	Sequence 47, Appl
7	42.0	11	US-08-401-512-15	Sequence 15, Appl
8	42.0	11	US-08-481-6588-73	Sequence 73, Appl
9	42.0	11	US-08-477-504A-73	Sequence 73, Appl
10	42.0	11	US-08-486-756A-73	Sequence 73, Appl
11	42.0	11	US-08-485-862B-73	Sequence 73, Appl
12	42.0	11	US-08-787-739-73	Sequence 73, Appl
13	42.0	11	US-08-487-077A-73	Sequence 73, Appl
14	42.0	11	US-08-485-863A-73	Sequence 73, Appl
15	42.0	11	US-08-485-049D-73	Sequence 73, Appl
16	42.0	11	US-08-118-115-73	Sequence 73, Appl
17	42.0	11	US-09-177-716-73	Sequence 73, Appl
18	42.0	11	US-09-772-719B-73	Sequence 73, Appl
19	40.0	10	US-08-049-283A-31	Sequence 31, Appl
20	40.0	10	US-08-049-283A-33	Sequence 33, Appl
21	40.0	10	US-09-508-753B-70	Sequence 70, Appl
22	37.0	9	US-08-437-013-6	Sequence 6, Appl
23	37.0	9	US-09-275-506A-6	Sequence 6, Appl
24	35.0	9	US-09-639-576-2	Sequence 19, Appl
25	35.0	8	US-08-593-345B-19	Sequence 19, Appl
26	35.0	8	US-08-859-954-55	Sequence 248, App
27	35.0	8	US-08-859-954-248	Sequence 249, App
28	35.0	8	US-08-859-954-249	Sequence 267, App
29	35.0	8	US-08-859-954-267	Sequence 406, App
30	35.0	8	US-08-859-954-406	Sequence 540, App
31	35.0	8	US-08-859-954-540	Sequence 6, Appl
32	35.0	8	US-08-855-372B-6	Sequence 6, Appl
33	35.0	8	US-09-498-851-6	Sequence 6, Appl

ALIGNMENTS

c	34	7	35.0	9	1	US-08-068-945A-36	Sequence 36, Appl
c	35	7	35.0	9	1	US-08-442-806-36	Sequence 36, Appl
c	36	7	35.0	9	1	US-09-063-450-10	Sequence 10, Appl

RESULT 1

US-09-862-847-15/c
Sequence 15, Application US/09862847
Patent No. 6593111
GENERAL INFORMATION:
APPLICANT: Baric, Ralph S.
APPLICANT: Boyd, Yount
TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
FILE REFERENCE: 5470.270
CURRENT APPLICATION NUMBER: US/09/862,847
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/206,537
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: US 60/285,320
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent version 3.1
SEQ ID NO 15
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

Query Match
Best Local Similarity 45.0%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1023 CCAGAGG 1033

Db 10 CCAGAGG 2

US-09-862-844-6/c
Sequence 6, Application US/09862844

Patent No. 6583986
GENERAL INFORMATION:

APPLICANT: Cai, Hong

APPLICANT: Keller, Richard

APPLICANT: Werner, James

APPLICANT: Goodwin, Peter

TITLE OF INVENTION: RAPID HAPLOTYPE BY SINGLE MOLECULE DETECTION

FILE REFERENCE: S-94,652

CURRENT APPLICATION NUMBER: US/09/862,844

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patent version 3.0

SEQ ID NO 6

LENGTH: 12

TYPE: DNA

ORGANISM: PNA probe MLGc5P

US-09-862-844-6

Query Match
Best Local Similarity 45.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1023 GCCCAGGA 1031

Db 10 GCCCAGGA 2

RESULT 3

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:40:33 : Search time 0.001 seconds
(without alignments)
83.680 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtgsg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 195 seqs, 2092 residues

Total number of hits satisfying chosen parameters: 390

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 195 summaries

Database: rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	20	1	AA162417	Human ABC transpor
2	12	60.0	15	ABA96458	Human IL-2 probe S
3	11.8	59.0	15	AA45928	IGFBP2 oligonucleo
4	11.4	57.0	15	AA45927	IGFBP2 oligonucleo
5	11.4	57.0	15	AA45928	IGFBP2 oligonucleo
6	11	55.0	13	ABC34320	Oligonucleotide SE
7	11	55.0	13	ABC34321	Oligonucleotide SE
8	11	55.0	13	ABC45614	Oligonucleotide SE
9	11	55.0	13	ABC45615	Oligonucleotide SE
10	10	50.0	10	AA261481	Metastatic breast
11	10	50.0	11	ABV70040	Human skin EST 782
12	10	50.0	11	ABV62619	Human skin EST 405
13	10	50.0	12	ABH76170	Oligonucleotide pr
14	10	50.0	12	ABH71877	Oligonucleotide pr
15	10	50.0	13	AAA54180	5' exon-intron jun
16	9.8	49.0	13	ABC48640	Oligonucleotide SE
17	9.8	49.0	13	ABC48641	Oligonucleotide SE
18	9.8	49.0	13	ABF28997	Oligonucleotide SE
19	9.8	49.0	13	ABF28996	Oligonucleotide SE
20	9.4	47.0	11	ABK95486	Human CYP3A5 gene
21	9.4	47.0	11	ADQ33668	Human facial skin-
22	9.4	47.0	12	ABH13302	Oligonucleotide pr
23	9.4	47.0	12	ABH17015	Oligonucleotide pr
24	9.4	47.0	12	ABH14555	Oligonucleotide pr
25	9.4	47.0	12	ABH16922	Oligonucleotide pr
26	9.4	47.0	12	ABH91427	Oligonucleotide pr
27	9.4	47.0	12	ABH61189	Oligonucleotide pr
28	9.4	47.0	12	ABH98731	Oligonucleotide pr
29	9.4	47.0	12	ABH85586	Oligonucleotide pr
30	9.4	47.0	12	ABF78633	Chromosomal abnorm
31	9	45.0	10	AAZ79882	Human dendritic ce
32	9	45.0	10	AAZ79850	Human dendritic ce
33	9	45.0	10	AAZ78803	Human dendritic ce

34	9	45.0	10	1	AA282426	Metastatic breast
35	9	45.0	10	1	AA422275	Yeast NORF gene SA
36	9	45.0	10	1	ABT14287	Nucleic acid PCR a
37	9	45.0	10	1	ADQ38610	Human CYP gene al
38	9	45.0	11	1	AA487795	Promoter P1583 tra
39	9	45.0	11	1	AA507926	Human transcriptio
40	9	45.0	11	1	ABV64418	Human skin EST 220
41	9	45.0	11	1	ABV71839	Human skin EST 962
42	9	45.0	11	1	ABV92970	P1584 promoter tra
43	9	45.0	11	1	AA521210	Transmissible gast
44	9	45.0	11	1	ADQ30775	Oligonucleotide pr
45	9	45.0	11	1	ADQ33660	Human facial skin-
46	9	45.0	12	1	ABH19388	Oligonucleotide pr
47	9	45.0	12	1	ABH108577	Oligonucleotide pr
48	9	45.0	12	1	ABH25588	Oligonucleotide pr
49	9	45.0	12	1	ABH13144	Oligonucleotide pr
50	9	45.0	12	1	ABH18769	Oligonucleotide pr
51	9	45.0	12	1	ABH88612	Oligonucleotide pr
52	9	45.0	12	1	ABH67143	Oligonucleotide pr
53	9	45.0	12	1	ABH94365	Oligonucleotide pr
54	9	45.0	12	1	ABH96358	Oligonucleotide pr
55	9	45.0	12	1	ABH74429	Oligonucleotide pr
56	9	45.0	12	1	ABH70993	Oligonucleotide pr
57	9	45.0	12	1	ABH88613	Oligonucleotide pr
58	9	45.0	12	1	ABH152693	Oligonucleotide pr
59	9	45.0	12	1	ABH140468	Oligonucleotide pr
60	9	45.0	12	1	ABH10163	Oligonucleotide pr
61	9	45.0	12	1	ABH94363	Oligonucleotide pr
62	9	45.0	12	1	ABH73341	Oligonucleotide pr
63	9	45.0	12	1	AA25619	MILC5L LNA probe
64	9	45.0	12	1	AA25617	MILC5P PNA probe
65	9	45.0	12	1	ADP28540	Human secreted pro
66	9	45.0	12	1	AA714161	Cytokine responsiv
67	8.4	42.0	10	1	AAV56888	Regulatory element
68	8.4	42.0	10	1	AAZ79653	Human dendritic ce
69	8.4	42.0	10	1	AAZ77834	Human dendritic ce
70	8.4	42.0	10	1	AAZ78009	Human dendritic ce
71	8.4	42.0	10	1	AAZ84938	Metastatic breast
72	8.4	42.0	10	1	AAZ85708	Metastatic breast
73	8.4	42.0	10	1	AAZ81181	Metastatic breast
74	8.4	42.0	10	1	AAZ80869	Metastatic breast
75	8.4	42.0	10	1	AAZ78893	Human dendritic ce
76	8.4	42.0	10	1	AA43656	Probe #25 for sequ
77	8.4	42.0	10	1	AAH63873	Human ubiquitously
78	8.4	42.0	10	1	AA43792	Yeast NORF gene SA
79	8.4	42.0	10	1	AA43723	Yeast NORF gene SA
80	8.4	42.0	10	1	AA438664	Yeast NORF gene SA
81	8.4	42.0	10	1	AA437520	Yeast NORF gene SA
82	8.4	42.0	10	1	AA437547	Yeast NORF gene SA
83	8.4	42.0	10	1	AA440919	Yeast NORF gene SA
84	8.4	42.0	10	1	AA438810	Yeast NORF gene SA
85	8.4	42.0	10	1	AA441899	Yeast NORF gene SA
86	8.4	42.0	10	1	AA440814	Yeast NORF gene SA
87	8.4	42.0	10	1	ABH88354	Human CHNE gene P
88	8.4	42.0	10	1	ABH37010	Human ALA52 gene a
89	8.4	42.0	10	1	ABH13516	Human E7F8 primer-
90	8.4	42.0	10	1	ABL52253	Human PKG2 prefer
91	8.4	42.0	10	1	ABL52252	Human PKG2 prefer
92	8.4	42.0	10	1	ABV78454	Human transcriptio
93	8.4	42.0	10	1	ABV84246	Human mitochondria
94	8.4	42.0	10	1	ABK23703	Transcript tag DNA
95	8.4	42.0	10	1	ABN84506	Rat smooth muscle
96	8.4	42.0	10	1	ACA60848	Human PKM2 gene po
97	8.4	42.0	10	1	ABQ72900	Human GATV gene p
98	8.4	42.0	10	1	ABK65537	Human GATV gene p
99	8.4	42.0	10	1	ACF04526	Stuffer sequence u
100	8.4	42.0	10	1	ADH13685	Cytoplasmic tumour
101	8.4	42.0	10	1	ADH169071	Human TAT protein-
102	8.4	42.0	10	1	ADM33249	Oligo SEQ ID 84, u
103	8.4	42.0	11	1	AAA16595	Human MN gene 5', u
104	8.4	42.0	11	1	AAA52514	Human MN gene intr
105	8.4	42.0	11	1	ABQ87504	Human skin stress/
106	8.4	42.0	11	1	ABQ87500	Human skin stress/

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:38:34 ; Search time 0.001 Seconds

(without alignments)
37.240 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20
Sequence: 1 cttccgcccaagaagtg95 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 88 seqs, 931 residues

Total number of hits satisfying chosen parameters: 176

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 88 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	15	1	BD061440
C 2	10	50.0	11	1	AX623364
C 3	10	50.0	11	1	AX630785
C 4	9.4	47.0	11	1	AX635700
C 5	9.4	47.0	11	1	AX472203
C 6	9	45.0	10	1	BD238992
C 7	9	45.0	10	1	BD239512
C 8	9	45.0	10	1	BD239813
C 9	9	45.0	11	1	AX635840
C 10	9	45.0	11	1	AX625163
C 11	9	45.0	11	1	AX632584
C 12	9	45.0	12	1	AX349259
C 13	9	45.0	12	1	AX349261
C 14	9	45.0	10	1	AX25869
C 15	8.4	42.0	10	1	AX043677
C 16	8.4	42.0	10	1	BD238844
C 17	8.4	42.0	10	1	BD239019
C 18	8.4	42.0	10	1	BD240663
C 19	8.4	42.0	10	1	COT66709
C 20	8.4	42.0	10	1	AR303500
C 21	8.4	42.0	10	1	AX152798
C 22	8.4	42.0	10	1	AX301616
C 23	8.4	42.0	10	1	AX374630
C 24	8.4	42.0	10	1	AX805907
C 25	8.4	42.0	10	1	BD161343
C 26	8.4	42.0	10	1	BD166511
C 27	8.4	42.0	11	1	AR074494
C 28	8.4	42.0	11	1	AR081174
C 29	8.4	42.0	11	1	AR081171
C 30	8.4	42.0	11	1	AR081119
C 31	8.4	42.0	11	1	AR081115
C 32	8.4	42.0	11	1	AR104278
C 33	8.4	42.0	11	1	AR143540

34	8.4	42.0	11	1	AR171446	ACCESSION:AR171446
35	8.4	42.0	11	1	AR171617	ACCESSION:AR171617
36	8.4	42.0	11	1	BD243207	ACCESSION:BD243207
37	8.4	42.0	11	1	BD243089	ACCESSION:BD243089
38	8.4	42.0	11	1	COT633231	ACCESSION:COT633231
39	8.4	42.0	11	1	COT635108	ACCESSION:COT635108
40	8.4	42.0	11	1	COT635129	ACCESSION:COT635129
41	8.4	42.0	11	1	COT636261	ACCESSION:COT636261
42	8.4	42.0	11	1	COT637368	ACCESSION:COT637368
43	8.4	42.0	11	1	COT637393	ACCESSION:COT637393
44	8.4	42.0	11	1	COT637792	ACCESSION:COT637792
45	8.4	42.0	11	1	134822	ACCESSION:134822
46	8.4	42.0	11	1	AX412934	ACCESSION:AX412934
47	8.4	42.0	11	1	AX470563	ACCESSION:AX470563
48	8.4	42.0	11	1	AX471678	ACCESSION:AX471678
49	8.4	42.0	11	1	AX471682	ACCESSION:AX471682
50	8.4	42.0	11	1	AX623377	ACCESSION:AX623377
51	8.4	42.0	11	1	AX623396	ACCESSION:AX623396
52	8.4	42.0	11	1	AX623509	ACCESSION:AX623509
53	8.4	42.0	11	1	AX625581	ACCESSION:AX625581
54	8.4	42.0	11	1	AX626059	ACCESSION:AX626059
55	8.4	42.0	11	1	AX626126	ACCESSION:AX626126
56	8.4	42.0	11	1	AX626949	ACCESSION:AX626949
57	8.4	42.0	11	1	AX627089	ACCESSION:AX627089
58	8.4	42.0	11	1	AX627751	ACCESSION:AX627751
59	8.4	42.0	11	1	AX627792	ACCESSION:AX627792
60	8.4	42.0	11	1	AX627837	ACCESSION:AX627837
61	8.4	42.0	11	1	AX628191	ACCESSION:AX628191
62	8.4	42.0	11	1	AX628263	ACCESSION:AX628263
63	8.4	42.0	11	1	AX629947	ACCESSION:AX629947
64	8.4	42.0	11	1	AX630798	ACCESSION:AX630798
65	8.4	42.0	11	1	AX630817	ACCESSION:AX630817
66	8.4	42.0	11	1	AX630930	ACCESSION:AX630930
67	8.4	42.0	11	1	AX632853	ACCESSION:AX632853
68	8.4	42.0	9	1	AX480947	ACCESSION:AX480947
69	8.4	42.0	9	1	AX668629	ACCESSION:AX668629
70	8.4	42.0	9	1	AX668630	ACCESSION:AX668630
71	8.4	42.0	9	1	AX668813	ACCESSION:AX668813
72	8.4	42.0	9	1	AX668814	ACCESSION:AX668814
73	8.4	42.0	9	1	AB012724	ACCESSION:AB012724
74	8.4	42.0	10	1	AX15662	ACCESSION:AX15662
75	8.4	42.0	10	1	BD238780	ACCESSION:BD238780
76	8.4	42.0	10	1	BD238878	ACCESSION:BD238878
77	8.4	42.0	10	1	BD238880	ACCESSION:BD238880
78	8.4	42.0	10	1	BD239283	ACCESSION:BD239283
79	8.4	42.0	10	1	BD239952	ACCESSION:BD239952
80	8.4	42.0	10	1	BD240374	ACCESSION:BD240374
81	8.4	42.0	10	1	BD240388	ACCESSION:BD240388
82	8.4	42.0	10	1	BD240561	ACCESSION:BD240561
83	8.4	42.0	10	1	119168	ACCESSION:119168
84	8.4	42.0	10	1	119170	ACCESSION:119170
85	8.4	42.0	10	1	AR303345	ACCESSION:AR303345
86	8.4	42.0	10	1	AX152217	ACCESSION:AX152217
87	8.4	42.0	10	1	AX153242	ACCESSION:AX153242
88	8.4	42.0	10	1	AX301610	ACCESSION:AX301610

ALIGNMENTS

RESULT 1
BD061440/c
LOCUS
DEFINITION
METHOD
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BD061440
Method for selectively separating living cell expressed with
specific gene.
BD061440
BD061440.1 GI:22607046
JP 2001286285-A/2.
synthetic construct
artificial sequences.
1 (bases 1 to 15)
Ishibashi, K. and Tsuji, A.

15 bp DNA linear
PART 27-AUG-2002